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### 09/913329 PCT/CA00/00147

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NEP1-HU	1 MGK	10 .sesqmdite	DINTPK	20 PKKKQRWT	'PLEI	30 s	) SLSVLVLLL
PEX-HUM	MEA	.ETGSS	VETGK	KANRGTRI	ALVV	F	VGGTLVLG
KELL-HU	MEGGDQSEE +	EPRERSQAGG	MGTLWSQI *	ESTPEERL	PVEGSRPWA	VARRV	LTAILIL.
ECE1-HU	MSTYKRATL	DEEDLVDSLS	EGDAYPN	GLQVNFHS	PRSGQRCWA	ARTQVEKRL	VVLVVLLA
conseris	M.		Т		Ρ		L
NEP1-HU	**	50 LYA.TYDD *	*	DCIKSAAR		** **	** **
PEX-HUM	TILFLVSQG	LLSLQAKQ	. EYCLKPE	ECIEAAAA	LSKVNLSV	DPCDNFFRF	ACDOWTEN

TILFLVSQGLLSLQAKQ...EYCLKPECIEAAAAILSKVNLSVDPCDNFFRFACDGWISN \* \* \* \* \* \* \* \* \* \* \*\* \*\* \*\* \*\*\* .GLLLCFSVLLFYNFQNCGPRPCETSVCLDLRDHYLASGNTSVAPCTDFFSFACG...RA KELL-HU \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* + AGLVACLAALGI.QYQTRSPSVCLSEACVSVTSSILSSMDPTVDPCHDFFSYACGGWIKA ECE1-HU consens L L C C L V PC DFF ACGGW

NEP1-HU	100 NVIPETSSRY	GNFD:	10 ILRDELEV	120 VLKD	13 VLQEPKTED			10 JYRSCINI	150 ESAIDSR
	* * * * *	*	* *	* *	* *			* ** *	
PEX-HUM	NPIPEDMPSY	GVYPI	WLRHNVDL	KLKE	LLEKSISRRRD	reai(	QKAKI I	YSSCMN	EKAIEKA
KELL-HU	VERNUS		*	+	* *		* *	* ***	*** *
NCDD-HU	KEINNS	rQi	LATKNKN	RLRR	ILEVQ.NSWHP			TYNSCMD	LA I EAA
ECE1-HU	NPVPDGHSRW	- (TFS)		ttvu	LLENS.TA.SVS		**	* **	**
	De ve Bonbrak	011.01	i Dia Pilité M	TIVU	LLENS.IA.SV	5 tALI	(KAQV)	YRACMNE	ETRIEEL
consens	N P (	G F	L	LK	LE	А	KA	Y SCMNE	E AIE

	160	170	180		190		200		
NEP1-HU	GGEPLLKLLPDI.YC	WPVATENW	EQKYGAS	5.WTAE	KAIAQLN	ISKYGKI	KVLIN	LFVG	TD
PEX-HUM	DAKPLLHILRHSPF			RESLI	* OTLATES	* COYSNI	+ + CVETE	+ +	* תם
	+ +		+ +	*	++ ++	**	* *	د ۷ توند. +	еD +
KELL-HU	GTGPLRQVIEEL	GGWRI	SGKWTSI	LN FN	RTLRLLM	ISQYGHI *	FPFFR	AYLG	РН
ECE1-HU	RAKPLMELIERL	GGWNI	TGPWAKI	DNFQ	DTLQVVI	AHYRTS	SPFFS	vrvs	AD
consens	PL		GW	F	TL	Y	F	YV	D

230 220 240 250 260 NEP1-HU DKNSVNHVIHIDQPRLGLPSR.DYYECTGIYKEACTAYVDFMISVARLIRQEERLPI.DE + PEX-HUM DKASNEHILKLDQATLSLAVREDYLDNSTEAKSYRDALYKFMVDTAVL....LGA.NS \*\* \* \* \* ++ ÷ PASPHTPVIQIDQPEFDVPLKQDQEQKI.YAQIFRE.YLTYLNQLGTL....LGG.DP KELL-HU \*\*\* \*\* ÷ 4 \*\* \* \*\*\* \* \* \* \* \* SKNSNSNVIQVDQSGLGLPSRDYYLNKTENEKVLTG.YLNYMVQLGKL.....LGGGDE ECE1-HU consens КS VI DQ L LP R DY Κ Y М L LG D

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NEP1-HU	2 - SELENCELENGKPFSWLNF
PEX-HUM	
KELL-HU	LINE LOCAL CONTRACT DOLKEMAPAIDWLSC
ECE1-HU	EAIRPQMQQILDFETALANITIPQEKRRDEELIYHKVTAAELQTLAPAINWLPF
consens	M E A PER KTLP WL
NEP1-HU	330 340 350 360 370 380 TNEIMSTVNISITNEEDVVVYAPEYLTKLKPILTKYSARDLQNLMSWRFIMDLVSS
PEX-HUM	*
KELL-HU	LQATFTPMSLSPSQSLVVHDVEYLKNMSQLVEEMLLKQRDFLQSHMILGLVVTLSPA
ECE1-HU	LNTIFYPVEINESEPIVVYDKEYLEQISTLINTTDRCLLNNYMIWNLVRKTSSF
consens	V L LNMWV
NEP1-HU	390 400 410 420 430 LSRTYKESRNAFRKALYGTT.SETATWRRCANYVNGNMENAVGRLYVEAAFAGESK
PEX-HUM	LSRRFQYRWLEFSRVIQGTT.TLLPQWDKCVNFIESALPYVVGKMFVDVYFOEDKK
KELL-HU	LDSQFQEARRKLSQKLRELTEQPPMPARPRWMKCVEETGTFFEPTLAALFVREAFGPSTR
ECE1-HU	LDQRFQDADEKFMEVMYGTKKTCLPRWKFCVSDTENNLGFALGPMFVKATFAEDSK
consens	L FQ F GT PWCV G FV F K
NEP1-HU	440 450 <u>460</u> 470 480 490 HVVEDLIAQIREVFIQTLD.DLTWMDAETKKRAEEKALAIKERIGYPDDIVSNDNKLNNE
PEX-HUM	EMMEELVEGVRWAFIDMLEKENEWMDAGTKRKAKEKARAVLAKVGYPE.FIMNDTHVNED
KELL-HU	SAAMKLFTAIRDALITRLR.NLPWMNEETONMAQDKVAQLQVEMGASE.WALKPELARQE
ECE1-HU	SIATEIILEIKKAFEESLS.TLKWMDEETRKSAKEKADAIYNMIGYPN.FIMDPKELDKV
ECE1-HU consens	

510 520 500 530 540 550 NEP1-HU YLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISGAAVVNAFYSSGRNQIVFP \* \*\* \* \* \* \* + \* \* \*\* \*\*\*\*\* \*\* \* \* \* LKAIKFSEADYFGNVLQTRKYLAQSDFFWLRKAVPKTEWFTNPTTVNAFYSASTNQIRFP PEX-HUM \* \* \* \* ÷ + \*\*\* \*\* \* \*\* KELL-HU YND.IQLGSSFLQSVLSCVRSLRARIVQSFLQPHPQHRWKVSPWDVNAYYSVSDHVVVFP + + \*\*\*\*\* \* \* \* ECE1-HU FNDYTAVPDLYFENAMRFFNFSWRVTADQLRKAPNRDQWSMTPPMVNAYYSPTKNE (2A/B) . consens YF N LRW P VNA YS N TVEP

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NEP1-HU	560 AGILQPPFFSA	570 QQ.SNSLN ++	580 YGGIGMVIG	590 HEITHGFDDN(	600 GRNFNKDGDLV	610 /DWWTQQSASNF
PEX-HUM	AGELQKPFFWG	TEYPRSLS	YGAIGVIVG	HEFTHGEDNN(	GRKYDKNGNLI	DPWWSTESEEKF
KELL-HU	AGLLQPPFFHP	GY.PRAVNI	FGAAGSIMA	HELLHIFYQL.	LLPGGCL.	ACDNHAL
ECE1-HU	AGILÇAPFYTR	SS.PKALNI	GGIGVVVG	HELTHAFDDQG	GREYDKDGNLF	PWWKNSSVEAF
consens	AG LQ PFF	P LN	G IG GI	HE TH FD G	R KGL	WW S F

620 630 640 650 660 670 NEP1-HU KEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQAYRAYQNYI..KKNG.EE \*\* \*\* \* \* \* \* \*\*\* + + \* \* \*\* KEKTKCMINQYSNYYWK.KAGLNVKGKRTLGENIADNGGLREAFRAYRKWINDRRQGLEE PEX-HUM + \* + \*\* \*\* \*\*\* \* \*\* \* \* \* QEAHLCLKRHYAAF..PLPSRTSFNDSLTFLENAADVGGLAIALQAYSKRL..LRHH.GE KELL-HU \* \* + ++ ++ +++ + ++ 4 - + KRQTECMVEQYSNY...SVNG.EPVNGRHTLGENIADNGGLKAAYRAYQNWV..KKNG.AE ECE1-HU ৢ ۲B) consens KE CM QY N NG TLGENIADNGGL A RAY G E

NEP1-HU	680	69	-	700	710	720	730
NEFI-NU	KLLPGLDLNH	4KQLFFLN *****	JFAQVWCG + + +	TYRPEYAVN	SIKTDVHSP	GNFRIIGTL	
PEX-HUM	PLLPGITFTN ++	NQLFFLS	YAHVRCN	SYRPEAARE		PQFRVNGAI	
KELL-HU	TVLPSLDLSE	QQIFFRS	YAQVMCR	KPSPQDSH.			* * SSTPAFARY
ECE1-HU	HSLPTLGLTN	INQLFFLG	FAQVWCS		GLITDPHSP	SRFRVIGSL	* * SNSKEFSEH
consens	LP L L	QLFFL	AQV C	PE	D HSP	FRV G L	SN EF

	740	750
NEP1-HU	FHCRKNSYMPEKK.	CRVW
	* * ++ ++	++ +
PEX-HUM	FNCPPNSTMNRGMDS	SCRLW
	* +  +	+ ++
KELL-HU	FRCARGALLNPSSR.	COLW
	*** * ++	+ +
ECE1-HU	FRCPPGSPMNPPHK.	CEVW
	<	(e)
consens	FC SMNP	C W

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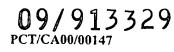
PRIMER	SEQUENCE
(IA)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CA-3'
(1B)	5'-TGGATGGAT/CGA/CIGG/AIACIA/CG-3'
(2A)	5'-A/GTIGTITTT/CCCIGCIGGIA/GT/AIC/TTA/TCA-3'
( <b>2B</b> )	5'-A/GTIGTITTT/CCCIGCIGGIA/GT/AIC/ITG/CCA-3'
(3)	5'-AIICCICCIA/TC/TA/GTCIGCIG/AC/TA/GTTT/CTC-3'
(4)	5'-GAT/CAAT/CT//CTIGAT/CGAA/GT//CTIAAT//CTGGATGG-3'
(5)	5'-T/CT/CACCAIATICT/GA/GCATCG/TT/CTTCATIGGG/ATG-3'

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# Sequence of NL-1 CDNA from mouse

ctget et acte accorgage ce toge consectes da sate cesares agent ta aggaet tge et gaet gaet gad ge acorgget ce cet ggg cat toge a tradage at tgag age agent a sage agent a sage at tgag age agent a sage agent a sage at tgag age agent a sage agent a sage agent a sage agent a sage at tgag agent agent

6556				5/	22				
sy egc	a 10 GCC GCC	60 Val GTT	90 130 20	120 ser TCC	0 4 0 0 4 0	180 175 AAA	210 83n AAC	4 H U 0 0 U	270 val GTG
, , , ,	91Y GGA (	thr . ACG 0	glu a GAA P	aan s Aac t	pro a CCG G	leu l Tta a	1eu a TTG A	91n p CAG CC	aer 2. TCA G
, 00 0 F	Leu CTG	arg ( AGG J	leu o crc o	thr d ACC P	агд р ССС С	val l GTC T	val l GTG T	830 9 670 09	thr s ACG T
ア ア サ リ	1eu TTG	glu a GAG 7	Ile J ATC C	glu t GAG A	his a car c	ser v AGC G	ala v GCT G	ile a Ata G	met t ATG A(
, , , ,	Leu CTG	asp Gar	arg 1 AGA 7	pro CCA G	gln h CAG C	leu s CTG A	leu a TTG G	tyr 1 TAC A	phe m TTC A
;	leu CTG	160 166	ala GCC J	ATC 0	3 e 1 100 0	leu l CTG C	gin l cag t	11e t ATC T	glu p GAG T
	Leu CTG	ser TCC	ala d GCT (	val J GTG P	thr s ACT J	pro 1 CCC C	arg g CGA C	val 1 GTC A	leu g CTG G
	Leu CTG	phe TTC	ala GCA (	his v	ser t TCC P	glu p Gag C	glu a GAG C	his v Car g	tyr 1 Tac C
	val GTG	his	ile ATA (	his h cac	asp GAT 1	Ser G TCT	leu g CTG G	акд ћ ССС С	ala t GCC T
	me t ATG	Leu CTA	val GTG	arg l AGG (	glu a GAG (	asp GAC 1	glu I GAA C	36r a AGC C	lys a AAA G
	leu CTG	leu CTG	cys TGT	Leu CTG	leu CTG	аг <u>д</u> АСА (	100 100 100	ser TCC P	arg l CGG A
	91 <i>Ү</i> 666	aer AGC	ser AGC	Чср ТСр	val GTG	lys AAG J	Lys t AAG 1	a an a AAC T	val a GTA C
	tyr TAT	thr ACT	pro CCA	91Y 66C	917 966	glu GAG	Leu CTC	gln a CAG J	Lys . AAG o
	glu GAG	leu TTA	thr ACC	gly ggà	Lys AAA	ATC	91Y 660	asp GAC 0	his l cac J
	val GTG	leu CTC	th <i>r</i> ACC	cys TGC	leu CTC	GTG	A HG	as GAD CAC	asn l
	phe TTC	pro CCC	суз ТСС	ala GCC	<b>11e</b> ATC	ser AGT	thr ACC	AAT	ASD
	91 <i>y</i> GGC	leu CTG	11e ATC	tyr TAC	val GTT	gln CAA	glu gag	trp 100	480 GAC
	pro CCA	gln CAG	asp GAC	gln CAG	glu GAG	asn AAC	Asn	41e ATC	glu GAG
	a e r TCC	1 y s PAG	ser AGT	tyr TAC	leu CTG	me t ATG	<b>t</b> rp ТGG	phe TTC	gln CAG
	1 ya AAG	91Y GGG	l y9 Aaa	phe TTC	glu Gag	с <u>у</u> з ТGC	1 ya AAG	Leu CTC	phe TTC
	lys AAG	11e ATA	Leu CTG	a a n AAC	asp GAC	3 er TCC	asp GAT	asp GAC	tyr TAT
	arg CGG	3 e r AGC	ser TCA	glu Gaa	arg CGG	arg CGC	Met ATG	11e ATC	tyr TAC
	CYS TGT	t yr TAC	ser TCA	cys TGT	leu CTG	tyr TAT	ala GCC	Leu CTC	glu Gag
	15G	phe TTC	dap GAT	pro CCC	11e ATC	Leu CTA	val GTG	val GTC	arg CGG
	1 91Y	VAL GTC	AGG	ABC	asp GAC	thr Aca	р <i>г</i> о ССТ	8 F G C G G	36r TCC
	I ala I GCA	917 66T	Leu CTC	AGG	phe TTT	l ys AAG	1 1 6 0 1 0 0	arg AGG	pro CCA
	l arg 3 AGA	r crg	y ala V GCC	3er TCG	GTC	ala GCC	91Y GGT	a s n AAC	me t ATG
	L glu 3 GAG	L thr 3 ACT	A CGA	gln CAA	36r 700	1 ys AAG	91y Gga	phe TTC	917 660
	t val 3 676	e val A GTG	L LYS AAA	c asp GAC	I tyr I TAC	glu GAG	Val GTA	gln CAG	1au TTG
	met 1 ATG	1 ATA	val GTA	met ATG	arg CGA	CTG	ATG	Rer TCG	thr ACC
		16	181	271	361	451	541	631	721

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300 h13	CAT 330 phe	TTT 360 val	010 190 val	420 Val	4 2 4 5 4 1 4 5 0 1 4 5 0			240 240	570 570 TTT
thr	ACG	AGG	leu Leu	510 510	646 9 8 8 0 8 8				
glu	glu glu	GAA val							
leu îmi	gln gln	glu glu							
91u	Leu Leu	glu Glu			-		-		
Leu Leu							-		
val		יים מיות היים מיות						-	•
alu glu		phe TTC	asn AAC					-	•
ala GCG	) 01 10 10 10 10	Leu CTG							-
met Atg	Met ATG	glu GAG		ala GCG			leu g TTG G	lys a Aag a	
glu GAG		val GTC	thr ACC	l ys AAG				leu l CTC A	
glu Gag		g L u G A A	arg CGG	arg CGC	ser TCC	leu ∂ CTG Q	tyr 1 TAC A		-
arg CGG			ala GCA	tyr TAC	917 917	aan 1 AAC o	asp t GAC 1	gln a CAG A	
Val GTG		3 e r TCT	ser TCA	asp GAC	val GTG	asp d GAT J	pro CCT 0	leu g CTT C	val a GTC A
met Atg	ala GCC	зег ТСТ	tyr TAC	val GTG	ala GCC	val GTG	tyr F TAC O	gly l GGA C	val v GTG G
ala GCC	thr ACT	leu TTG	8 er AGC	årg CGT	aer AGC	phe TTT	917 1 660 1	aan g AAC G	ala v GCA G
AGC AGC	val GTC	val GTG	asp Gat	ala GCG	glu GAG	val GTG	ATT (	glu g GAG J	ala d GCT (
glu GAG	asp GAT	a sn AAC	11e Att	glu GAG	met ATG	36r TCC	gln CAG	phe TTT (	914 666
Lys AAG	h1s CAT	gln Caa	11e ATC	Lys AAA	asn AAC	arg AGG	glu GAA	tyr TAT	ATC 0
TCC	arg AGG	11e ATA		pha TTC	aer AGT	41e ATA	arg CGG	Leu CTG	ATC
Leu CTG	LYS AAA	phe TTC	glu GAG	arg Aga	asn AAC	lys AAG	11e ATA	a s p GAC	1 1 G G
asn Bac	glu GAG	1eu CTC	Leu CTG	gln cag	val GTC	glu GAG	asn AAT	glu GAG	Leu CTC
gln CAG	gln CAG	thr ACT	AST	ser AGC	tyr TAT	11a ATT	met ATG	суг ТАТ	asn AAT
a a b GAC	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	н П С С Г С С Г	glu GAG	leu CTG	aer AGC	leu CTG	ala GCC	phe TTC	gln CAG
J Lys 3 AAA	C VAL V GTC	AAC	Leu CTG	36r AGC	val GTC	glu GAG	Lys AAG	thr ACT	asp GAC
l arg r AGG	thr ACA	phe TTT	TAC	91Y 660	суз TGT	arg AGA	glu GAA	leu TTG	val GTG
r leu G CTT	ala GCC	917 666		ATT ATT	glu GAG	val GTC	gln CAG	ser AGT	1yb AAG
r met T ATG	a asn c AAC	Lys AAG		cGA	arg CGA		ala GCC	аен ПОС	glu gaa
a thr C ACT	GCC GCC	r ctg		I GAT	trp TGG		l ys Aag	tуr TAC	arg CGG
ala I GCC	leu CTG	917 1 667		L CTA				glu gaa	Leu CTT
118	106	166	1081	1171	1261	1351	1441	1531	1621

rorrago "caretoco"

7/22 750 CYB TGC b1s CAC phe TTC ala GCB

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600 91u 630 pha TTC 660 leu CTC 690 690 720 91n CAG pro arg gly ser pro met his pro met lys arg cys arg ile trp \*\*\* CCA CGA GGC AGC CCC ATG CAC CCC ATG AAG CGA TGT CGC ATC TGG TAG CCAAGGCTGAGGCTATGCTGCGGGCCCAGCGCCAGCGCAGGGCTTCGCGAATG 2473 CIGCGCCCCCTCAGGCCAGTGAGGGTCAGCAGCCGGGAAGAGCAGTCAGCTGCCTTCCACCCTCCATAGTGTGTGGGCTAAAGGCTTCAGACTTGAGCTAAGTAAACGC his cac CAC thr ACC arg CGA val 510 91Y 666 Arg CGG ser AGT gln CAG ala GCC 11e ATT ala GCC phe TTC asp GAT phe TTC Met val 1 ATG GTG 7 ser TCG 91Y 66A glu GAG Ly3 AAA glu GAG TTC TCT phe TTC asn AAC 917 667 pro CCG AGT AAC tyr arg | TAT AGG ( gly ile gly GGC ATC GGG val GTG 917 920 asn AAT asp GAT 91Y 660 t rp TGG gln CAG ala GCT ser TCC asn leu pro AAC CTG CCA 91Y 666 ដំពូ ដំពូ leu CTG a s n AAC 917 666 phe TTT asp GAC asp GAC trp TGG cys TGT ser leu asn TCC TTG AAT 1eu CTG ala GCA arg CGG trp TGG ser leu gln TCA CTA CAG met ATG Leu CTA Leu CTA tyr ala gln val TAT GCC CAG GTG a an AAC glu GAA туг ТАС pro ala gly ile leu gln pro pro phe phe ser lys asp gln pro gln CCA GCA GGG ATT CTC CAG CCG CCC TTC TTC AGC AAG GAC CAA CCA CAG phe asp lys asn gly TTT GAC AAG AAC GGC trp 166 ala GCT 91y 660 tyr lys TAC AAG CTG CTG ser TCT 765 gln tyr gly asn phe CAG TAC GGC AAC TTC asn AAC gln ala CAG GCA tyr arg TAC AGG phe ile TTC ATC arg asn p CGT AAC T leu phe | CTT TTC CTT AAG arg val GTG Ile tyr ATC TAT gln CAG 91у 661 91*У* 667 pro CCT asn AAT 91У 66А ala GCC 3er AGT met ATG asp GAT asn AAC tyr TAT asp val his GAC GTC CAC glu asn ile ala asp GAG AAC ATT GCC GAC asp GAT cγs TGC gly leu asn leu thr GGA CTG AAC CTG ACC gln gln ser gln CAG CAG TCG CAA phe TTT his gly r cac goc ile lys thr ATC AAG ACG 110 thr ATC ACA 91Y 666 pro CCG 36r TCC ЩC 1711 1981 2251 1801 1891 2071 2161 2925

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Sequence of NL-2 cDNA from humans

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				ρ	100			$\sim$	
28 1 thr	910 58 670	8 H 0	118 his CAC		/ <i>22</i>	8 n 9	e s u	α μυ	8 4 9 8
L val	to bu d pu c PC c PC				er gl	0 6 50 0 7 0			1 91n 6 CAG 328
n leu tri	TTA CI TTA CI					- U	ссс ССС ССС ССС ССС ССС ССС		
l n u	i and The c				9 91Y 66C		s e A G	169	
Leu leu CTC CTC C	s phe TTC		p leu G CTG	l leu 5 CTG	s arg CGA		r ser		
eu le Graa			trp 166	a val GTG	I Lys AAG	glu GAG	asn AAC		
	leu	Pro	, 91 <i>Y</i>	ala	glu	Leu	gln	lys	gln
	CTG	CCT	660	GCG	GAG	CTC	CAG	AAG	CAG
eu Le	arg	thr	91 y	lys	ile	91Y	asp	arg	val
CTC	CGG	ACC	GGA	AAA	ATA	6GA	GAC	CGG	GTG
y gly leu leu leu leu	Ser	thr	cys	leu	val	val	asp	a s n	Leu
GGG CTG CTG CTG C	AGC	ACC	TGC	CTC	GTG	GTA	GAC	A A C	CTG
y le	ala	ςys	ala	ile	ser	thr	asn	ser	cys
CrG	GCT	TGC	GCA	ATC	AGT	ACC	AAC	AGC	TGC
у <u></u> д1	Leu	val	phe	val	gln	glu	t rp	91Y	Ser
ССС	CTT	GTC	TTT	GTC	CAG	GAG	TGG	66C	AGC
u gly	arg	glu	g1n	glu	asn	asn	ile	д1у	GAC
GGG G	CGC	GAG	CAG	GAG	AAC	AAC	ATC	660	
u glu	pro	ser	tyr	leu	met	t rp	phe	asn	arg
GAG GG	CCA	AGC	TAC	CTG	ATG	TGG	TTC	AAC	AGG
crge Crge	leu CTG	Val GTG	phe TTC	glu GAG	cγs TGC	arg AGG	leu CTC	phe TTC	0 7 7 7 7 7 7 7
i arg pro gly phe	gln	glu	asp	asp	ser	asp	asp	TAC	leu
CGC CCG GGG TTC (	CAG	GAG	GAC	GAC	TCC	GAC	GAC		CTG
0 g13	lys	gln	asp	arg	arg	me t	ile	tyr	asn
	AAG	caa	GAC	CGC	CGC	ATG	ATC	TAC	AAC (
L L L L L L L L L L L L L L L L L L L	д1 <i>ү</i>	ala	cys	Leu	tyr	ala	Leu	glu	ala
	666	GCC	TGT	CTC	TAC	GCG	CTC	GAG	GCA 1
CGC .	arg AGA	glu GAG	pro CCG	val GTC	leu CTG	val GTG	val GTC (	arg CGN	GAT
1 1ys	arg	pro	glu	asp	thr	0000	arg	ser	glu g
AAG	CGC	CCA	GAA	GAC	ACG		CGC	TCC	GAG (
'glr	asp	ile	thr	phe	AGG	trp	arg	010	arg
CAG	GAC	ATC	ACG	TTT		100	AGG	010	CGG
66G	ala	917	thr	ile	ala	914	AAC	met	Leu a
66G	GCC	666	ACC	ATC	GCC	66C		ATG (	CTG 0
r ala	tуr	arg	pro	ser	lys	gly	phe a	917 n	leu l
GCA	TAC	CGA	CCG	AGC	AAG	GGA (		GGC 7	TTG 0
met val glu ser ala gly arg ala gly gln lys	Leu	pro	asp	tyr	glu	val o	gln g	leu	thr 1
ATG GTG GAG AGC GCC GGC CGT GCA GGG CAG AAG (	CTC	CCC	GAC	TAC	GAG	GTG (	CAG 1	TTG (	ACG 1
91у	val	l ys	Met	arg	val	val	ser o	thr 1	ala
66С	GTC	Ada	ATG	AGA	GTG	GTG (	TCA O	ACC 1	GCC P
ala	gly	arg lys	asn	ser .	ala	glu d	asn s	pro	val a
GCC	GGT	CGA AAA	AAC	TCA	GCT (	GAG O	AAC T	CCC A	GTG G
ser	leu	val lys	gln	asn	pro	Tro 0	met a	gln p	ser v
AGC	TTG	GTA AAA	cag	AAC	CCG		ATG A	cag c	TCA G
glu	ala	val	Leu	thr	arg I	ile l	Leu d	asp g	val s
GAG	GCC	GTA	CTC	ACC		ATC 1	CTG P	GAC C	GTG T
val	val	phe	ile	glu 1	asp	asp i	ala l	ile a	met v
GTG	GTG	TTT	ATC (	GAG 1	GAC (	GAC P	GCG C	ATA G	ATG G
me t ATG	CTG	ACC	AGG	Dr.O CCT CCT	lys AAG G	Leu d CTG G	leu a CTG G	tyr i TAC A	TTC A
000	ala	arg	ala	ile F	ala l	leu l	gln l	ile c	gln p
	GCC (	AGG J	GCC /	ATC C	GCC A	CTG C	CAG C	ATC T	CAG T
GTG (	ala	glu a	ala d	val i	thr a	pro	arg g	ile i	Leu g
	GCT (	GAG J	GCC C	GTG A	ACT G	CCC C	CGG C	ATC A	CTG C
T (	916	181 0	271 C	361 G	451 A	541 C	631 C	i 721 A	811 C
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9/22 arg AGG 478 leu CTG 358 1eu CTG 388 phe asn 418 508 glu AAC TTT 448 glγ 000 GAG 538 pro CCA 598 ile 914 660 568 **ATT** 628 gln CAG 91Y 66A Leu CTG leu CTG val GTC Leu CTG glu GAG 010 val 30F TCC 91Y 660 met ATG lys AAG ile ATA ala GCG tyr TAC glu CAC Leu CTG Lys AAG TAC TAC 475 67λ arg CGG ile ATC thr ACC L y s AAG leu CTC asp GAC ile ATC leu CTC phe phe TTT his CAC l ys AAA arg AGG arg CGC ser TCC lau CTG tүr TAC aan AAC asn AAC ala GCG tyr TAC val GTC ala GCC tуr TAC 91У 66С thr Acc asp GAC gln AAT 1eu TTG leu TTG ser TCT ser TCA asn AAC val GTG glu GAG pro CCT Leu CrG ala GCC val GTC ala GCC ser TCC tуr TAC val GTG ala GCC val GTG his CAC 36r AGT val GTG d be ile ATC Leu CTA thr ACC arg CGA asn AAC phe TTT 91<u>ү</u> 666 asn AAC a La GCG er to CCA val GTC val GTG asp GAC thr ACA glu GAG val GTG ile ATC glu GAG ala GCG gln asp GAC thr ACT ile ATC asp GAC met ATG thr ACA gla phe TTT 91Y 666 glu GAG his CAC gln caa ile ATC Lys AAG asn AAC arg CGG glu GAG tyr TAC ile ATC LY3 AAG агд Адд ile ATA asn AAC phe TTC ser AGC val GTG arg CGG Leu CTG ile Arc ser AGC glu GAG phe TTC glu GAA arg AGA asn AAC Lys AAG ile ATC asp GAC ដូក ដូក្ល phe TTC glu GAG leu CTG gln CAG val GTC leu CTT asp GAC ser AGC glu GAG Leu CTC pha TTC gln CAG thr ACT asn AAC tуr TAC ser AGC ile ATT aet ATG 36r TCA AAT Pro CCC pro CCC CCC ե*ւ*թ 166 gln CAG leu CTA 91*Y* 660 leu CTC ala GCC phe TTC ors CCA or CC Dro val GTA asn AAC leu CTG ser AGC val GTG glu Lys AAG asn AAC gln CAG asp GAC thr ACG phe TTT туг ТАС 91Y GGT cys TGT arg AGA glu GAG leu CTG val GTG Leu CTC ala GCC 917 667 o U U U U U U ile ATT g Lu GAA val GTC gln asn AAT Lys AAG ile ATC lys AAG 1ys AAG arg CGC ile ATC arg CGT Met ala GCG 30H TCC glu GAA 91Y 666 ala GCC Leu CTG 917 660 asp GAC н гср ССр ser AGC 1ys AAG tуr ТАС ala GCC arg CGG Leu CTG g1y GGC гуг ТАТ Leu CTG arg CGC 1ys AAG 1ys AAG glu GAG leu CTT pro CCH gln CAG phe val GTC val GTG val GTG ser AGC lγs AAG Ly3 AAG phe glu GAG thr ACA gln CAG Leu CTG GTG glu GAG asp GAC ser TCC asp GAC Val GTA arg glu GAG ser AGC glu GAG val GTG arg 91у 66д glu GAG gln ile CAG ATT leu CTG leu CTC leu CTG g Ln CAA glu GAA trp TGG val GTG pro CCT glu GAG arg CCC 38r AGC glu GAG glu GàG met ATG Leu CTG GTC phe TTC a 3 p CAC asn AAC arg CGG arg AGG Leu CTG glu GAG asp GAT leu CTG thr ACA ala GCG Bet ATG asn AAC gIn CAG arg CGA Val GTT glu GAG Pro CCA туг ТАС 917 660 glu GAG me t ATG 19 19 19 asn AAC ala GCC 106 1081 1171 1261 166 1351 1441 1531 1621 1711

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10/22 **365 AGT** 658 asn AAC 688 glu GAG 718 **tуr TAC** 748 ala GCC GIG 0 C C C AAG GGA ដ្ឋដ្ gIn ğ ala GCA ser TCC ala 200 GCT CAT CCT TTC ដូរ ដូរ glu me t ATG 91Y GGG Leu CTG 000 GTA AAC CCA CCC asp GAT asp CAC trp TGG Cγs TGC asn AAC GCA 200 AGG CCC TGC Met met ATG ATG a S lys AAG g ln CAG trp TGG 000 AGT 10 10 leu CTG leu CTC val GTG Leu CTG 000 U U U U TCC AAC tуг ТАС asp GAC gln CAG ser TCG CCA 000 GTG 610 010 91Y 660 ala GCC TAG ដូរី ala GCC 91У 666 ter CGT GCA ACT asn AAT tyr lys TAT AAG a B C C C туг ТАТ trp 100 GTA Leu CTG 770 TGA TAG AGA CAA TCA AAA asp lys cac aag l 174 194 Val GTA asn AAC val GTG AGT **400** TTT CAA AGA AAA asn AAC ala GCC ile ATC arg AGG arg CGC CGA CCC CAG phe TTC 917 667 gln cAA phe TTC tуr ТАС αys TGC ACC asn AAC TAC TAC arg CGG phe TTC 000 1 ys AAG CTG arg CGA GAC arg CGG g la Cac val GTG TAG Leu CTC Leu CTG glu Gag CCT ACA GCT TCA GAA CTT GAG CTA AGT AAA TGC ACA ACT 91Y 660 ty. 91Y 666 gln 1ys AAG AGC 010 CTG GAC AAT ile ATC TGC 91<u>у</u> 66**3** g Lu GAG pro CCC ser AGT CAC GTC met ATG asn AAC his CAT his CAC AGG his CAC AGC 200 asp GAC 10.73 10.73 asp GAC thr ACC Met ATG CGA TGC val GTC 200 phe TTT glu GAG ala GCT Leu CTC GTG asp GAC pro CCC 900 AGT 91Y 660 39r TCA ile ATT asp GAT thr ACA CTA thr ACC TCT CTC his CAC gIn CNG asn AAC Leu CTG lγs AAG 91Y 66C GCA 000 000 thr ACG glu GAG glu GAA 91Y 66C ile ATC arg GAG 000 CCC CCT ile Arc arg CGG 91Y 666 pro CCC ser TCC ala GCC TCG 200 glu GAG phe TTC gln CAA leu CTT leu CTG cγs TGT TGC TCT TCT ACA chi CAC gln CAG his CAC kh Kh ile ATC his CAC 202 000 CAG CCA GTA 91Y 666 gln CAG asn AAC ala GCC gln CAG CAG phe TTC CCC ACC TCA CTC ATC thr ACC phe TTC asp GAC thr ACG phe TTC TGC CCT CTT B B L glu GAG 977 5 l ys AAG asp GAC ACG U U U U U TGT me t ATG phe TTC aan AAC 917 660 pro CC 0 ala GCA CCT GAG CAT 91y 660 000 asn val GTG 91*y* 667 000 arg phe TTC AAG GTG 1801 1891 1981 2071 2341 2431 2521 2161 2251 2611

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11/22 808 i GTC 22 22 52 52 1eu CTG 82 Jeu CTC 112 leu CTG 142 asp GAC 172 Рго ССТ 202 leu CTA 000 CAG Ser AGC 917 666 ala GCC or o CC o phe TTC 917 660 Met ATG leu CTG ile ATC arg AGG ala GCC GCT 500 val GTG Leu CTG Ser arg CGC ile 91Y GGT arg CGG val GTC tуr ТАС leu CTG 0000 616 туг ТАС arg CGG met ATG ala GCT ala GCC 91Y 666 arg CGA asn tуr ТАС ala GCA gln 0000 CAG lys AAG ala GCC ala GCT ala GCC his CAC o C C C C C C C C C pro CCG Leu CTC ala GCA arg gln CAG TCA 220 val GTC 91У 666 ala GCG arg arg CGC arg CGG 91Y 66C asp GAC ser TCG Leu CTG glu GAG GTA 000 000 glu GAG Leu CTG thr ACC ala GCG årg CGG ala GCG leu CTG 100 100 ser TCC val GTC val GTG GCT 22 gln ala GCC ile ATT phe TTC leu CTG leu CTG arg arg CGA asn AAC lys AAG gln CAA 000 CAT phe TTC Ser AGC ala GCC ala GCC trp TGG Leu CTG glu GAG ala GCG arg AGG glu GAG leu CTG 500 CGA glu GAG cγs TGC arg CGC lys AAG 91y GGT arg CGC ile ATC ala GCG asp GAC ser AGT ile ATC 000 CAC asp GAT ala GCG leu CTC arg CGC 91Y 660 arg CGG glu GAG asp GAC asp GAC val GTC glu GAG TCG 000 tyr TAC ala GCT 917 660 glu GAG leu CTA cys TGC arg CGC 917 666 Leu CTG gln CAA glu GAG 000 00 00 his CAC 91γ 66C ala GCC pro CCT ala GCC arg CGC met ATG o C C C C C C C C C C C C ser AGC asp GAT ala GCC 200 000 ala GCG leu TTG ala GCC с<u>у</u>s 160 phe TTC glu GAG asp GAC val GTC gln cAG arg CGT 1 ys AAG GAG 000 thr ACG phe TTC 91γ 66C ser TCG glu GAG leu CTC glu GAG thr ACG ala GCT gln CAG TCA GAG leu CTG phe TTC val GTG glu GAG tyr TAC asn glu GAG cys TGC leu CTC leu CTC glu GAA 200 CAC ser TCG 91Y 66C leu CTG pro CCC phe TTC gln CAA ser TCG ala GCG ser TCG tуг ТАС val GTG 160 000 гуг ТАТ or o CC O 91Y 666 cys TGT asp GAC glu GAG arg CGC phe TTC Leu CTG ala GCT 91Y 660 GAG 0000 pro CCG pro CCC ser TCG ala GCC gln CAG 91y 660 phe TTC Leu CTC thr ACC 917 660 a sp GAC CTC 500 orc CCC Dr leu CTG leu CTG 91Y 660 cys TGC ile ATC phe TTC leu CTG ala GCG arg AGG ala GCA 0000 CAT glu GAG ser TCC leu CTG g1y GGC pro CCA ala GCA asp GAC ala GCC glu GAG ala GCC 91*y* 667 GCT 000 me t ATG ala GCC cγs TGC 917 660 a s p GAC ala GCG arg CGC t r p TGG pro CCA leu CTG ala GCC CAG 917 660 000 val GTG ala GCC ile ATC ile ATC val GTG 91Y 66C ser AGC leu CTG leu CTC ACG 200 000 arg CGC glu GAG ala GCG ser AGC thr ACC l ys AAG 91У 666 tуr ТАС thr ACC Ser AGC 000 000 100 ala GCG arg CGC val GTC ala GCC 91y 66c arg CGC cys TGC val GTG leu CTC leu CTC 010 CAC 200 arg CGG pro CCG giry GGC asp GAC tyr TAT gln CAG asp GAC 917 660 917 666 val GTG AGA 000 500 91Y 666 asn AAC 91y 660 leu CTG thr ACC ala GCC glu GAG gln CAG asp GAT arg CGA 000 TGC 500 ala GCG trp 166 leu CTG asn AAC Leu CTC ala GCG ile ATC ala GCG gln CAG glu Gag GCT ACC ACC 967 927 927 arg t'J'T TAC ala GCC l y s AAG 91Y 66C val GTC Lys AAG asp GAC met ATG 000 200 100 o 10 U U l ys AAG cys TGC ala GCC asp GAC 91Y 66C ile ATT glu GAG TAC phe TTC -61 81 271 361 451 541 631 811 166 901 1081 721

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352 CCC CCC				gln Glac		glu GAG	562 ACG	Leu CTG	
thr	tуr	glu	ςys	gln	ala	his	36r	thr	trp
ACC	TAC	GAA	TGC	G CA(	GCC	CAT	TCC	ACC	166
ile	asp	ser	val	val	arg	val	lys	pro	asp
ATC	GAC	AGT	GTC	GT(	CGG	GTC	AAG	CCC	GAC
lys	thr	leu	arg	1ys	ala	glu	asp	gln	asp
AAG	ACA	CTG	CGG	C AA(	GCT	GàG	GAC	CAG	GAC
gln	ala	val	ala	ala	ala	рћа	val	Leu	tyr
CAG	GCG	GTC	GCC	GCC	GCT	ттт	GTG	CrG	TAC
leu	leu	val	Leu	lys	ala	glu	glu	ile	д1 <u>ү</u>
CTG	CTG	GTG	CTG	C AAJ	GCT	GàG	GAG	ATC	660
gln	leu	val	glu	ser	агд	τуr	gln	200	bid
CAG	CTG	GTG	GAG	AGC	АСС	тат	cAG	ДТБ	CAC
д1У	val	val	gln	ala	thr	glu	arg	ala	thr
666	GTG	GTG	CAG	GCC	Acc	GAG	CGG	GCG	ACC
leu CTG	val GTG	arg CGC	pro CCA	ala GC1	glu GAG	Lys AAG	ile ATT	5 CC 0 CC 0 CC 0 CC 0 CC 0 CC 0 CC 0 CC	Lau CTG
thr	glu	trp	l y s	ser	ala	asp	1Y3	phe	glu
ACG	GAG	TGG	AAG	CTCP	GCC	GAC	AAG	TTC	GAG
val	glu	val	asp	phe	a sp	val	1ys	val	his
GTG	GAG	GTG	GAC	C TTC	GAC	GTG	Aag	GTG	CAT
lys	glu	leu	ser	his	me t	ala	val	ale t	91 <i>ү</i>
AAG	GAA	CTG	AGC	5 CAC	Atg	GCT	GTT	Atg	ССА
a s n AAC	glu GAG	tyr TAC	91Y GGC	gly ala leu phe val his glu his phe ser ala ala ser lys ala lys val gln 3 GGC GCC CTC TTT GTA CAT GAG CAC TTC TCA GCT GCC AGC AAA GCC AAG GTG CAG	100 100 100	asp GAT	36F TCA	gln CAG	ile ATT
tуг ТАС	ser TCA	asn AAC	g l u GAG	his A CAT	a s p GAC	р но ССС ССС	lau CTC	asn AAC	ile Arc
me t	phe	his	me t	val	leu	1γ5	gln	1ys	thr
ATG	TTC	CAC	ATG	r GTJ	CTG	AAA	CAG	AAG	ACC
ser	asp	leu	glu	phe	glu	Leu	ile	asn	д17
TCC	GAC	CTG	GAG	C TT	GAG	CTG	ATC	AAC	660
ser AGC	glu GAG	val GTC	gln CAG	leu CTC	glu GAG	leu CTG	39r AGC	р н о С С С О С С С О	ile ATC
val	gln	arg	ala	ala	lau	phe	phe	Leu	g l y
GTC	CAG	CGG	GCA	C GC(	CTG	TTC	TTC	CTA	GGC
asp	phe	his	Leu	91У	arg	a sp	arg	tyr	91у
GAT	TTC	CAC	CTG	Т 66	CGC	CAC	CCC	TAT	666
arg	ile	рr0	glu	leu	gln	pro	ile	tуг	tyr
CGA	ATC	ССС	GAG	G CTT	CAG	CCG	ATC	TAC	TAC
arg	gln	thr	his	ala	91Y	tyr	36r	ala	asn
CGG	CAG	ACA	CAC	GGC	66C	TAC	AGC	GCC	AAC
leu	asp	ser	glu ala leu	met	ile leu	<u>д</u> 1у	авл	asn	Leu
CTA	GAC	TCC	GAG GCA CTG	C AT	ATC CTG	660	ААС	AAT	CTC
asp	leu	arg	ala	91У	ile	met val	leu	Leu	HOT
GAC	CTA	CGC	GCA	СС	ATC	ATG GTC	TTG	CTC	TOT
asp	leu	ile	glu	phe	ile lys tyr		asn ile 1	ala	gln
GAC	CTG	ATC	GAG	C TT	ATC AAG TAC		AAC ATC 7	GCG	CAG
tyr TAT	trp TGG	Leu CTC	arg CGT	his c cA	1 ys Aag	crc u	asn AAC	g1n CAG	0 H U U U U
glu	Lys	gln	phe	агд	ile	Bet	lys	Pro	phe
GAG		CAG	TTC	Т СС	ATC	ATG	Aag	CCA	TTC
ser TCA	trp 766	Ser TCG	pro CCA	asn C AA	asp GAC	me c ATG	рће ттс	р н О С С С С С С С С	asp GAC
c val GTG	cgg	crg	D L C C C C C C C C C C C C C C C C C C	G GC	glu Gaa	tyr TAC	tyr Tac	Leu CTC	рно ССН ССН
thr ACT	TTG	gln CAG	TCC	gln C CA	val GTG	gln CAG	thr ACC	Leu CTG	asp CAC
ile	his	gln	leu	gly gln ala asn arg his phe gly met ala	leu	Leu	1ys	100	tyr
L ATC	CAC	CAG	CTG	1531 GGC CAG GCC AAT CGC CAC TTT GGC ATG GCG	CTÀ	CTC	AAG	100	TAC
1171	1261	1351	1441	153	1621	1711	1801	1891	1981
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					/22				
arg CGT			142 TYF TAC	772 cYs TGT	222	GAG	GCT		
val GTC	lys AAG	phe TTC	his cac	Lys AAG	GCA	CTG	CAG		
ile ATC	lau CTC	leu CTC	glu GAG	his CAC	CAT	000	TGC		
с <u>у</u> з ТGC	91 <u>У</u> 66С	d In CAC	pro CCT	ala GCC	AGG	AGG	crc		
glu GAG	<u>д</u> 1у 660	asp GAC	ala GCC	pro CCT	200	AGG	ACC		
ala GCT	me t ATG	his CAT	his CAT	AAC	000	TTC /	CAG V		
1ys AAG	asp GAT	k K	1yg AAG	ATG	TAC (	CAC	200	AAA P	
arg CGN	a la GCB	H LA	a 8 p CAC	0 H C C C C D H C	000	CCT	000	TTA P	
leu CTG	ile ATC	1ys AAG	thr	Ser J	GCT	000	TAA C	CTG 1	
рре ТРС	AAC	Leu CTC	leu 1 CTG 1	val s GTC 1	ccr o	GCT G	CTC T	gca c	
arg CGC	glu GAG	arg CCC	val GTG	LY3 -	ccr c	ccr g	CTG C	ACT G	
39r AGC	917 666		gln d CAG	pro l CCA J	TCA C	0 000	ATT C	ATC A	
The state	Leu CTT	Leu J CTT (	Leu CTG (	суз г тот	GAA 1	GGT C	CAG A	TAA A	
H C C H	thr ACG	pro CCP	TAC	his CAC 3	CAC 0	0000		AAA T	
ala GCC	his CAC	his CAC	ile ATC	Ieu h TTA (	0000	GGA C	GGT O	GTC A	
glu	Lys AAA	glu   GAG	aer TCC	CTT 7	0 000	cca o	TGG 0	010	
thr ACG	g1Y GGG	pro CCA	gln	arg CGG	CTG (	CCT	TAC 1	AGT O	
ដ្ឋដ្	азп	91Y 66C	39L TCG	91Y 660	cca e	000	ATA 1	GCA A	
ដ្ឋដ្	val GTG	his	arg	phe	200	CCA	GAA I	GCT (	
his CAC	arg CGG	glu GAG	arg CGG	glu GAG	ACG	CTT (	AGG (	CTT (	
leu CTG	gln CAG	arg CGG	1ys Aag	glu GAG	TGC	TGC	GTG /	GTT (	
leu CTG	agn AAC	val GTG	ile ATC	phe TTT	225	ACC	GCT	TGT (	
asn AAC	tyr TAC	រី ដូ	с <u>у</u> з 760	gln cAG	000		000	000	
д1у 666	val GTC	1y3 AAG	ដ្ឋិដ្ឋ	a a r TCC	CTG	GGC ACC		CTT (	
TCA	thr ACT	gln CAG	asn AAC	val GTG	TGG	CTG	CTT	CAC	
arg CGC	phe	tyr TAT	gln	ser AGT	222	GCT	GGA CTT TGG	000	
asp GAC	asn AAC	ala GCC	ala GCC	91Y 66C	ter TGA	200	GCT	222 225	
tyr TAT	a s p GAC	FI D	phe TTT	Leu CTG 775	ដ្ឋដ្	AGC	GAG	TAC	
gln CAG	tуr TAT	TAC	ala GCC	val GTG	val GTG	000	GGT	TTG	
д1 <u>ү</u> 660	Leu CTC	ala GCC	ile Att	AGG	100 100	GGT	CAG	. 455	
2071	2161	2251	2341	2431	2521	2611	2701	2791 (	
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Sequence comparison between NEP, NL1, NL2 and NL3

NEP-HUM	1 MG	10 KSESQMDITDINTI	20 PKPKKKQRW	30 TPLEISLSVLVI	40 LLLTIIAV
	7			* *	+
NL1-MOU	MV **	ERAGWCRKKSPGF <sup>1</sup> * ** * ***	VEYGLMVLL	LLLLGAIVTLG	.VFYSI.GKQL
NL2-HUM	MV	ESAGRAGQKRPGF1	LEGGLLLLL	LLVTAALVALG	/LYADRRGKQL
NL3-HUM	MEPPYSLTAHYDEF	QEVKYVSRCGAGGA	ARGASLPPG	FPLGAARSATGA	ARSGLPRWNRREV

NEP-HUM	50	60		70	
NEF-HOM	TMIALYATYDD	GICKSS	DCIKSA	ARLIQ	NMDATT
NL1-MOU	PLLTSLLHFSWDERTVVKRALRDSSL		SCVIA	ARILE	NMDQSR
NL2-HUM	PRLASRLCFLQEERTFVKRKPRGIPEAQEV		GCVIA		NMDPTT
NL3-HUM	CLLSGLVFAAGLCAILAAMLALKYLGPVAAGGGAC	PEGCPER	KAFARA	ARFLA	NLDASI

	80	90	100	110	120	130	
NEP-HUM	EPCTDFFK	YACGGWLKR	NVIPETSSRY	GNFDILRDEL	EVVLKDVLQ	EPKTEDIVAVQ.KA	ł
			**** ***	* ******	** ** **	** **	•
NL1-MOU	NPCENFYQ	YACGGWLRH ******	HVIPETNSRY	SVFDILRDEL	EVILKGVLEI	DSTSQHRPAVE.KA	ł
NL2-HUM	EPCDDFYQ		HVIPETNSRY	SIFDVLRDEL		ISTAKDRPAVE.KA	ł
NL3-HUM	DPCQDFYS	FACGGWLRR	HAIPDDKLTY	GTIAAIGEQN		* * RPGGGPGGAAQRKV	1

	140	150	160	170	180	190
NEP-HUM	KALYRSCI	NESAIDSRG	GEPLLKLLPD:	IYGWPVATEN	IWEQKYGASWTAI	EKAIAQLNSKYG
		* * * *	**** +	* * * * *	* * *	* * * * *
NL1-MOU	KTLYRSCM	<b>\QSVIEKRD</b>	SEPLLSVLKM	/GGWPVAMDk	WNETMGLKWEL	ERQLAVLNSQFN
NL2-HUM						ERQLALMNSQFN
NL3-HUM	RAFFRSCLI	OMREIERLG	PRPMLEVIEDO	CGGWDLGGAE		NRLLYKAQGVYS

	200	210	220	230	240	250
NEP-HUM	KKVLINLF	VGTDDKNSVN	HVIHIDQPR	LGLPSRDYYEC	TGIYKEACTA	YVDFMISVARLI
	*** **	** **	*** ****	** *** **	+	* ** ***
NL1-MOU	RRVLIDLF *******	IWNDDQNSSR ******	HVIYIDQPT1 + +++++++	LGMPSREYYFQ	EDNNHKVRKA	YLEFMTSVATML
NL2-HUM	RRVLIDLF	IWNDDQNSSR	HIIYIDQPTI	LGMPSREYYFN	GGSNRKVREA	YLQFMVSVATLL
NL3-HUM	AAALFSLT				QDEDSEKV	LAAYRVFMERVL

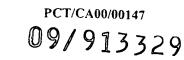
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	260	270	280	290	3	00	310
NEP-HUM	RQEERLPI	DENQLALEMN	KVMELEKEI/	NATAKP	EDRNDPML	LYNKMTL	AOIONNEST.
	* +	* *	* * * ÷ • •	****	* * *	** * *	* + +
NL1-MOU	RKDQNLSK * * **	ESAMVREEMA	EVLELETHLA	NATVPQ	EKRHDVTA	LYHRMDL	MELQERFGL
NL2-HUM	REDANLPR	DSCLVQEDMV *	QVLELETQLA	KATVPQ	EERHDVIA	LYHRMGL	EELQSQFGL
NL3-HUM	SLLGA	DAVEQKAQ	EILQVEQQLA	WITVSEYDI	DLRRDVSS	MYNKVTL	GQLQKITP.

	320	330	340	350	360	370
NEP-HUM	EINGKPFSWL	NFTNEIMSTV	NISITNEED	<b>VVVYAPEYLTK</b>	LKPILTKYS	ARDLQNLMSWR
	* * *	* * *	+	**** **	* * **	** ** **
NL1-MOU	••••KGFNWT	LFIQNVLSSV **** *****	EVELFPDEE	///YGIPYLEN	LEDIIDSYS	ARTMQNYLVWR
NL2-HUM				VVVYGI PYLQN	LENIIDTYS.	ARTIQNYLVWR
NL3-HUM	HLRWKT	VLLDQIF			+ VSQLIRSTP:	+ ++++++ HRVLHNYLVWR

	380	390	400	410	420	430
NEP-HUM	FIMDLVSSLSP	RTYKESRNAF	RKALYGTTSE	TATWRRCANY	VNGNMENAVO	RLYVEAAFAG
	* ***	** *	*******		** *** ***	** **
NL1-MOU	LVLDRIGSLS(	QRFKEARVDY	RKALYGTTVE	CEVRWRECVSY	VNSNMESAVO	SLYIKRAFSK
NL2-HUM	LVLDRIGSLS¢	QRFKDTRVNY	RKALFGTMVE	EVRWRECVGY		SLYVREAFPG
NL3-HUM	VVVVLSEHLSE	PFREALHEL	AQEMEGSDKP	QELARVCLGQ	ANRHFGMALG	ALFVHEHFSA

	440	450	460	470	480	490
NEP-HUM	ESKHVVEDLIA	AQIREVFIQ1	LDDLTWMDAE	TKKRAEEKAL	AIKERIGYPI	DIVSNDNK.L
NL1-MOU	DSKSTVRELIE	EKIRSVEVDN	LDELNWMDEE.	SKKKAOEKAM	NTREOIGYPT	YTTEDNNKHT
NL2-HUM	DSKSMVRELII					
NL3-HUM	ASKAKVQQLVE	EDIKYILGQF	LEELDWMDAE	TRAAARAKLQ	YMMVMVGYPD	

500 510 520 530 540 550 NEP-HUM NNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISGAAVVNAFYSSGRNQI \*\* \* \*\* \*\*\*\* \*\*\*\* \*\*\*\*\* \*\* \*\*\*\*\*\*\* \* \* \* \* NL1-MOU DEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQI \*\*\*\*\* \* \* \*\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* NL2-HUM DEEYSNLNFSEDLYFENSLQNLKVGAQRSLRKLREKVDPNLWIIGAAVVNAFYSPNRNQI ÷ + \* \*\* \* \* \* \* \* \* \*\* \* \*\* \* \*\* \*\* NL3-HUM DKE.YEFEVHEKTYFKNILNSIRFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQM

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	560	570	580	590	600	610
NEP-HUM	VFPAGILQPPF:	FSAQQSNSLN ** * ***	YGGIGMVIGH	EITHGFDDNC	PNENKOCDIV	DWWTQQSAS
NL1-MOU	VFPAGILQPPF	FSKDQPQSLN	FGGIGMVIGH		GRNFDKNGNML	DURICUISCES
NL2-HUM	VFPAGILQPPF1 *******	FSKEQPQALNI	FGGIGMVIGH	EITHGFDDNG	RNEDKNGNMM	DWWSNFSTQ
NL3-HUM	VFPAGILQPTLY	DPDFPQSLN	YGGIGTIIGH	ELTHGYDDWG		HWWTFDSVS

	620	630	640	650	660	670
NEP-HUM	NFKEQSQCMVY	QYGNFSWDL	AGGQHLNGINT	LGENIADNGG	JCOAVRAVON	UTKKNCEEV
			* * ** 4	********	***	+
NL1-MOU	HFQQQSQCMIY ** ** ****	QYGNFSWELA	ADNQNVNGFS1	CLGENIADNGG	VRQAYKAYLRI	VLADGGKDQ
NL2-HUM	HFREQSECMIY	QYGNYSWDLA • •	ADEQNVNGFNT	LGENIADNGG	VROAYKAYI.KW	MAEGGKDQ
NL3-HUM	RFLRKAECIVR	LYDNFTV	TYNQRVNGKHT	LGENIADMGG	LKLAYHAYQKV	IVREHGPEH

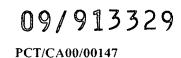
	680	690	700	710	720	730
NEP-HUM	LLPGLDLNHKQ	LFFLNFAQVW(	CGTYRPEYAN	ANSIKTDVHSE	CHEDITCHIO	NSAEFSEAF
NL1-MOU	RLPGLNLTYAQ	LFFINYAOVW	GSYRPEFAL	0SIKTDVHSE	IKYDVICSIO	NLPGFSEAF
NL2-HUM	QLPGLDLTHEQ	LFFINYAQVW	CGSYRPEFAI	QSIKTDVHSP	·····	++ + + NLAAFADTF
NL3-HUM	PLPRLKYTHDQ		+ +	** * *	* * * * * *	+

	740	750
NEP-HUM	HCRKNSYMNPEKK	CRVW
	** * * * *	* * *
NL1-MOU	HCPRGSPMHPMKR	CRIW
	** ** **** *	** +
NL2-HUM	HCARGTPMHPKER	CRVW
	** ** *	* **
NL3-HUM	HCPKVSPMNPAHK	CSVW



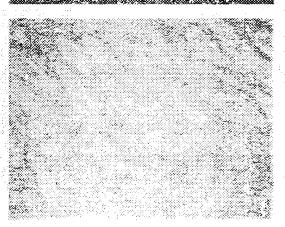






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## NL1 in the TESTIS





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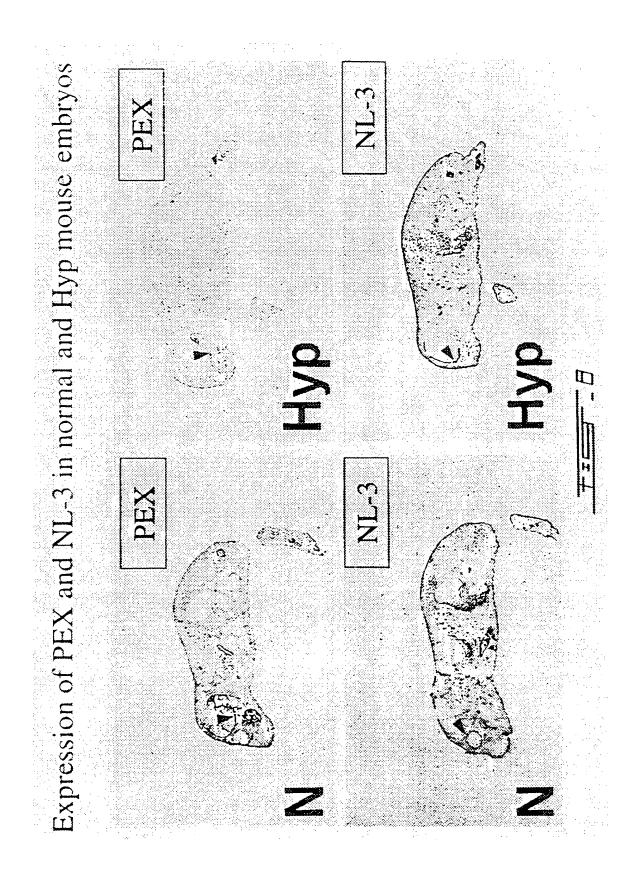
### SUBSTITUTE SHEET (RULE 26)





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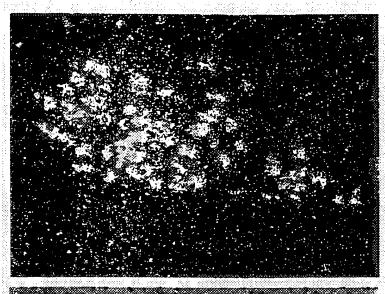


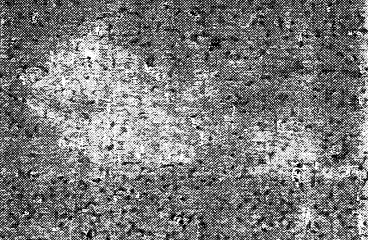




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19/22 NL3 in the BRAIN

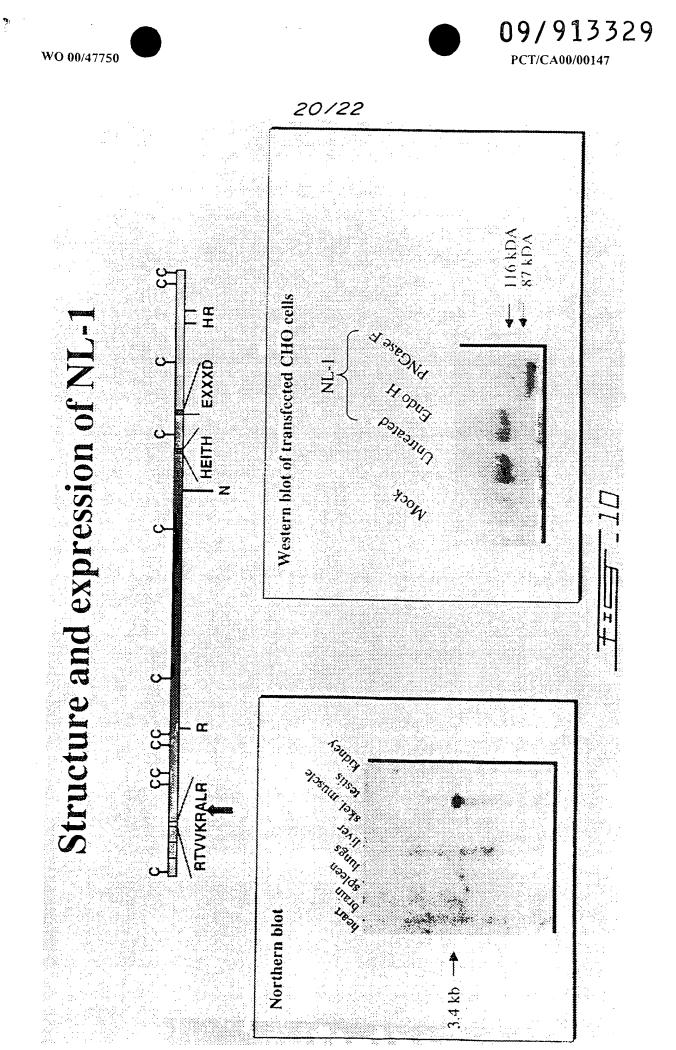






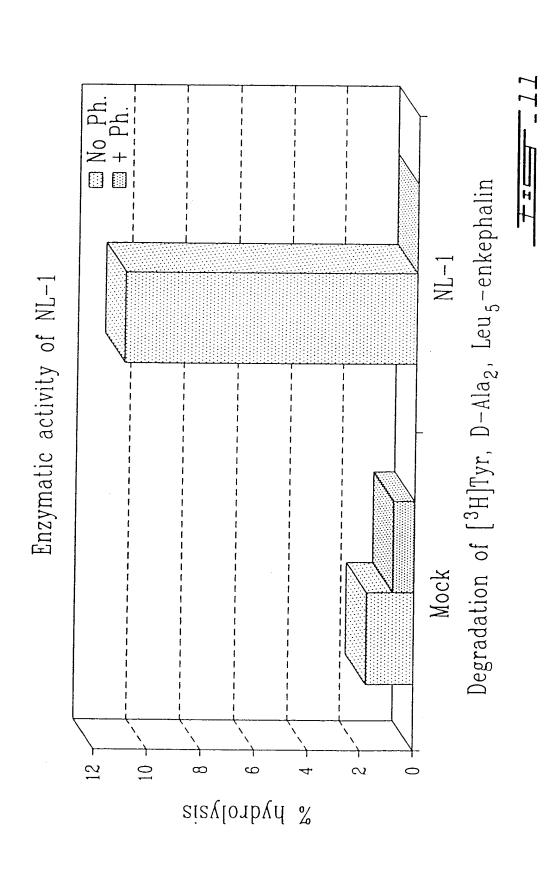
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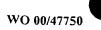




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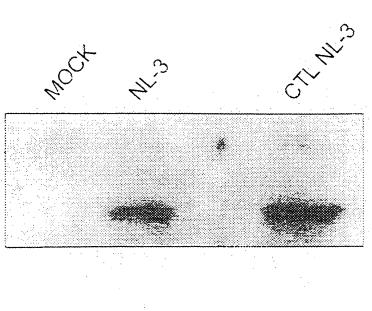
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